

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

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(i) APPLICANT: BRUCK, CLAUDINE

(ii) TITLE OF THE INVENTION: VACCINE

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(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: SmithKline Beecham

(B) STREET: 2 New Horizons Court, Great West Road, B

(C) CITY: Middx

(D) STATE:

(E) COUNTRY: UK

(F) ZIP: TW8 9EP

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

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(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

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(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

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(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Dalton, Marcus J

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: B45124

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: 0181 9756348

(B) TELEFAX: 0181 9756177

(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

Protein D 1/3 E7 His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys

1 5 10 15

Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro

20 25 30

Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp

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35 40 45

Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val

		50					55					60					
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe	
	65					70					75					80	
5	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr	
					85					90					95		
	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met	
				100					105					110			
	Ala	Met	His	Gly	Asp	Thr	Pro	Thr	Leu	His	Glu	Tyr	Met	Leu	Asp	Leu	
			115					120					125				
10	Gln	Pro	Glu	Thr	Thr	Asp	Leu	Tyr	Cys	Tyr	Glu	Gln	Leu	Asn	Asp	Ser	
		130					135					140					
	Ser	Glu	Glu	Glu	Asp	Glu	Ile	Asp	Gly	Pro	Ala	Gly	Gln	Ala	Glu	Pro	
	145					150					155					160	
	Asp	Arg	Ala	His	Tyr	Asn	Ile	Val	Thr	Phe	Cys	Cys	Lys	Cys	Asp	Ser	
15					165					170					175		
	Thr	Leu	Arg	Leu	Cys	Val	Gln	Ser	Thr	His	Val	Asp	Ile	Arg	Thr	Leu	
				180					185					190			
	Glu	Asp	Leu	Leu	Met	Gly	Thr	Leu	Gly	Ile	Val	Cys	Pro	Ile	Cys	Ser	
			195					200					205				
20	Gln	Lys	Pro	Thr	Ser	Gly	His	His	His	His	His	His					
		210					215					220					

(2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Protein D 1/3 E7 his

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35	60	ATTGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAATC
	120	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA
	180	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT
40	240	CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC
	300	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT
	360	CAAAGTTTAG	AAATGACAGA	AAACTTTGAA	ACCATGGCCA	TGCATGGAGA	TACACCTACA
45	420	TTGCATGAAT	ATATGTTAGA	TTTGCAACCA	GAGACAACTG	ATCTCTACTG	TTATGAGCAA
	480	TTAAATGACA	GCTCAGAGGA	GGAGGATGAA	ATAGATGGTC	CAGCTGGACA	AGCAGAACCG
50	540	GACAGAGCCC	ATTACAATAT	TGTAACCTTT	TGTTGCAAGT	GTGACTCTAC	GCTTCGGTTG
	600	TGCGTACAAA	GCACACACGT	AGACATTTCGT	ACTTTGGAAG	ACCTGTTAAT	GGGCACACTA
	660	GGAATTGTGT	GCCCCATCTG	TTCTCAGAAA	CCAAGTAGTG	GCCACCATCA	CCATCACCAT
55	663	TAA					

(2) INFORMATION FOR SEQ ID NO:3:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Protein D 1/3 E6 His/HPV 16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC  
 60 ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTACCAGAGC ATACGTTAGA ATCTAAAGCA  
 120 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT  
 180 CGTTTAGTGG TTATTCACGA TCACTTTTTA GATGGCTTGA CTGATGTTGC GAAAAAATTC  
 240 CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT  
 300 CAAAGTTTAG AAATGACAGA AAACCTTGAA ACCATGGCCA TGTTTCAGGA CCCACAGGAG  
 15 360 CGACCCAGAA AGTTACCACA GTTATGCACA GAGCTGCAAA CAACTATACA TGATATAATA  
 420 TTAGAATGTG TGTACTGCAA GCAACAGTTA CTGCGACGTG AGGTATATGA CTTTGCTTTT  
 480 CGGGATTTAT GCATAGTATA TAGAGATGGG AATCCATATG CTGTATGTGA TAAATGTTTA  
 20 540 AAGTTTATT CTAAAATTAG TGAGTATAGA CATTATTGTT ATAGTTTGTA TGGAAACAACA  
 600 TTAGAACAGC AATACAACAA ACCGTTGTGT GATTGTGTTAA TTAGGTGTAT TAACTGTCAA  
 25 660 AAGCCACTGT GTCCTGAAGA AAAGCAAAGA CATCTGGACA AAAAGCAAAG ATTCCATAAT  
 720 ATAAGGGGTC GGTGGACCGG TCGATGTATG TCTTGTTGCA GATCATCAAG AACACGTAGA  
 780 GAAACCCAGC TGACTIONTGG CCACCATCAC CATCACCATT AA  
 30 822

## (2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 40 Protein D 1/3 E6 His/HPV 16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

45 Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys  
 1 5 10 15  
 Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro  
 20 25 30  
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp  
 35 40 45  
 50 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val  
 50 55 60  
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe  
 65 70 75 80  
 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr  
 55 85 90 95  
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met  
 100 105 110  
 Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu  
 115 120 125  
 60 Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val  
 130 135 140  
 Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe  
 145 150 155 160  
 Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys  
 65 165 170 175  
 Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr

180 190  
 Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro  
 195 200 205  
 Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys  
 210 215 220  
 Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn  
 225 230 235 240  
 Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser  
 245 250 255  
 10 Arg Thr Arg Arg Glu Thr Gln Leu Thr Ser Gly His His His His His  
 260 265 270  
 His

15 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 Protein D 1/3 E6/E7/ HPV16

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC  
 60  
 ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTACCAGAGC ATACGTTAGA ATCTAAAGCA  
 120  
 30 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT  
 180  
 CGTTTAGTGG TTATTCACGA TCACTTTTGA GATGGCTTGA CTGATGTTGC GAAAAAATTC  
 240  
 CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT  
 35 300  
 CAAAGTTTAG AAATGACAGA AACTTTGAA ACCATGGCCA TGTTTCAGGA CCCACAGGAG  
 360  
 CGACCCAGAA AGTTACCACA GTTATGCACA GAGCTGCAA CAACTATACA TGATATAATA  
 420  
 40 TTAGAATGTG TGTACTGCAA GCAACAGTTA CTGCGAGGTG AGGTATATGA CTTTGCTTTT  
 480  
 CGGGATTTAT GCATAGTATA TAGAGATGGG AATCCATATG CTGTATGTGA TAAATGTTTA  
 540  
 AAGTTTTATT CTAAAATTAG TGAGTATAGA CATTATTGTT ATAGTTTGTA TGGAACAACA  
 45 600  
 TTAGAACAGC AATACAACAA ACCGTTGTGT GATTTGTTAA TTAGGTGTAT TAACTGTCAA  
 660  
 AAGCCACTGT GTCCTGAAGA AAAGCAAAGA CATCTGGACA AAAAGCAAAG ATTCCATAAT  
 720  
 50 ATAAGGGGTC GGTGGACCGG TCGATGTATG TCTTGTGCA GATCATCAAG AACACGTAGA  
 780  
 GAAACCCAGC TGATGCATGG AGATACACCT ACATTGCATG AATATATGTT AGATTGCAA  
 840  
 CCAGAGACAA CTGATCTCTA CTGTTATGAG CAATTAAATG ACAGCTCAGA GGAGGAGGAT  
 55 900  
 GAAATAGATG GTCCAGCTGG ACAAGCAGAA CCGGACAGAG CCCATTACAA TATTGTAACC  
 960  
 TTTTGTGCA AGTGTGACTC TACGCTTCGG TTGTGCGTAC AAAGCACACA CGTAGACATT  
 1020  
 60 CGTACTTTGG AAGACCTGTT AATGGGCACA CTAGGAATTG TGTGCCCCAT CTGTTCTCAG  
 1080  
 AAACCAACTA GTGGCCACCA TCACCATCAC CATTAA  
 1116

65 (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 Protein D 1/3 E6/E7/ HPV16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10 Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys  
 1 5 10 15  
 Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro  
 20 25 30  
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Ala Asp  
 35 40 45  
 15 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val  
 50 55 60  
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe  
 65 70 75 80  
 20 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr  
 85 90 95  
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met  
 100 105 110  
 25 Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro Gln Leu  
 115 120 125  
 Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu Cys Val  
 130 135 140  
 Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe Ala Phe  
 145 150 155 160  
 30 Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala Val Cys  
 165 170 175  
 Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg His Tyr  
 180 185 190  
 Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn Lys Pro  
 195 200 205  
 35 Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro Leu Cys  
 210 215 220  
 Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn  
 225 230 235 240  
 40 Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser  
 245 250 255  
 Arg Thr Arg Arg Glu Thr Gln Leu Met His Gly Asp Thr Pro Thr Leu  
 260 265 270  
 His Glu Tyr Met Leu Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys  
 275 280 285  
 45 Tyr Glu Gln Leu Asn Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly  
 290 295 300  
 Pro Ala Gly Gln Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr  
 305 310 315 320  
 50 Phe Cys Cys Lys Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr  
 325 330 335  
 His Val Asp Ile Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly  
 340 345 350  
 55 Ile Val Cys Pro Ile Cys Ser Gln Lys Pro Thr Ser Gly His His His  
 355 360 365  
 His His His  
 370

## (2) INFORMATION FOR SEQ ID NO:7:

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 Protein D 1/3 E7 mutated HPV 16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 ATGGATCCAA GCAGCCATTC ATCAAATATG GCGAATACCC AAATGAAATC AGACAAAATC  
 60 ATTATTGCTC ACCGTGGTGC TAGCGGTTAT TTAGCAGAGC ATACGTTAGA ATCTAAAGCA  
 120 CTTGCGTTTG CACAACAGGC TGATTATTTA GAGCAAGATT TAGCAATGAC TAAGGATGGT  
 180 CGTTTAGTGG TTATTCACGA TCACTTTTTA GATGGCTTGA CTGATGTTGC GAAAAAATTC  
 240 CCACATCGTC ATCGTAAAGA TGGCCGTTAC TATGTCATCG ACTTTACCTT AAAAGAAATT  
 300 CAAAGTTTAG AAATGACAGA AAACTTTGAA ACCATGGCCA TGCATGGAGA TACACCTACA  
 15 360 TTGCATGAAT ATATGTTAGA TTTGCAACCA GAGACAACTG ATCTCTACGG TTATCAGCAA  
 420 TTAAATGACA GCTCAGAGGA GGAGGATGAA ATAGATGGTC CAGCTGGACA AGCAGAACCG  
 480 GACAGAGCCC ATTACAATAT TGTAACCTTT TGTGCAAGT GTGACTCTAC GCTTCGGTTG  
 20 540 TCGGTACAAA GCACACACGT AGACATTCGT ACTTTGGAAG ACCTGTTAAT GGGCACACTA  
 600 GGAATTGTGT GCCCCATCTG TTCTCAGAAA CCAACTAGTG GCCACCATCA CCATCACCAT  
 25 660 TAA  
 663

## (2) INFORMATION FOR SEQ ID NO:8:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: linear

Protein D 1/3 E7 mutated HPV 16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

40 Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys  
 1 5 10 15  
 Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro  
 20 25 30  
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp  
 35 40 45  
 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val  
 50 55 60  
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe  
 65 70 75 80  
 50 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr  
 85 90 95  
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met  
 100 105 110  
 Ala Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu  
 115 120 125  
 55 Gln Pro Glu Thr Thr Asp Leu Tyr Gly Tyr Gln Gln Leu Asn Asp Ser  
 130 135 140  
 Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro  
 145 150 155 160  
 60 Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser  
 165 170 175  
 Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu  
 180 185 190  
 Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser  
 195 200 205  
 65 Gln Lys Pro Thr Ser Gly His His His His His His

210

215

220

## (2) INFORMATION FOR SEQ ID NO:9:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 CLYTA E6 His HPV 16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC  
 15 60  
 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG  
 120  
 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG  
 180  
 20 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC  
 240  
 AAGTACAAGG ACACTTGGTA CTACTTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC  
 300  
 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA  
 25 360  
 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGGCATGT TTCAGGACCC ACAGGAGCGA  
 420  
 CCCAGAAAGT TACCACAGTT ATGCACAGAG CTGCAAACAA CTATACATGA TATAATATTA  
 480  
 30 GAATGTGTGT ACTGCAAGCA ACAGTTACTG CGACGTGAGG TATATGACTT TGCTTTTCGG  
 540  
 GATTTATGCA TAGTATATAG AGATGGGAAT CCATATGCTG TATGTGATAA ATGTTTAAAG  
 600  
 TTTTATTCTA AAATTAGTGA GTATAGACAT TATTGTTATA GTTTGTATGG AACAACTTA  
 35 660  
 GAACAGCAAT ACAACAAACC GTTGTGTGAT TTGTTAATTA GGTGTATTAA CTGTCAAAG  
 720  
 CCACTGTGTC CTGAAGAAAA GCAAAGACAT CTGGACAAAA AGCAAAGATT CCATAATATA  
 780  
 40 AGGGGTCGGT GGACCGGTCG ATGTATGTCT TGTGTCAGAT CATCAAGAAC ACGTAGAGAA  
 840  
 ACCCAGCTGA CTAGTGGCCA CCATCACCAT CACCATTAA  
 879

## 45 (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 CLYTA E6 His HPV 16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

55 Met Lys Gly Gly Ile Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 60 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met

85 90 95  
 Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr Tyr  
 100 105 110  
 5 Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Leu Ala Ser Met  
 115 120 125  
 Leu Asp Met Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu  
 130 135 140  
 Pro Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu  
 145 150 155 160  
 10 Glu Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp  
 165 170 175  
 Phe Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr  
 180 185 190  
 15 Ala Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr  
 195 200 205  
 Arg His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr  
 210 215 220  
 Asn Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys  
 225 230 235 240  
 20 Pro Leu Cys Pro Glu Glu Lys Gln Arg His Leu Asp Lys Lys Gln Arg  
 245 250 255  
 Phe His Asn Ile Arg Gly Arg Trp Thr Gly Arg Cys Met Ser Cys Cys  
 260 265 270  
 25 Arg Ser Ser Arg Thr Arg Arg Glu Thr Gln Leu Thr Ser Gly His His  
 275 280 285  
 His His His His  
 290

## (2) INFORMATION FOR SEQ ID NO:11:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

CLYTA E7 HIS HPV 16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40 ATGAAAGGGG GAATTGTACA TTCAGACGGG TCTTATCCAA AAGACAAGTT TGAGAAAATC  
 60 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG  
 120 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG  
 45 180 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC  
 240 AAGTACAAGG ACACTTGGTA CTA CTCTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC  
 300 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA  
 50 360 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGCCATGC ATGGAGATAC ACCTACATTG  
 420 CATGAATATA TGTTAGATTT GCAACCAGAG ACAACTGATC TCTACTGTTA TGAGCAATTA  
 55 480 AATGACAGCT CAGAGGAGGA GGATGAAATA GATGGTCCAG CTGGACAAGC AGAACCGGAC  
 540 AGAGCCCATT ACAATATTGT AACCTTTTGT TGCAAGTGTG ACTCTACGCT TCGGTTGTGC  
 600 GTACAAAGCA CACACGTAGA CATTCTGACT TTGGAAGACC TGTTAATGGG CACACTAGGA  
 660 ATTGTGTGCC CCATCTGTTC TCAGAAACCA ACTAGTGGCC ACCATCACCA TCACCATTAA  
 720

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## (2) INFORMATION FOR SEQ ID NO:12:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 CLYTA E7 HIS HPV 16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 Met Lys Gly Gly Ile Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys  
 1 5 10 15  
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 15 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 20 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr Tyr  
 100 105 110  
 Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Leu Ala Ser Met  
 115 120 125  
 25 Leu Asp Met Ala Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met  
 130 135 140  
 Leu Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu  
 145 150 155 160  
 30 Asn Asp Ser Ser Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln  
 165 170 175  
 Ala Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys  
 180 185 190  
 Cys Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile  
 195 200 205  
 35 Arg Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro  
 210 215 220  
 Ile Cys Ser Gln Lys Pro Thr Ser Gly His His His His His His  
 225 230 235

40

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 CLYTA E6E7 His HPV16

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

50 ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC  
 60  
 AATGGCACTT GGTACTACTT TGACAGTICA GGCTATATGC TTGCAGACCG CTGGAGGAAG  
 55 120  
 CACACAGACG GCAACTGGTA CTGGTTGGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG  
 180  
 AAAATCGCTG ATAAGTGGTA CTATTTC AAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC  
 240  
 60 AAGTACAAGG ACACTTGGTA CTA CTAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC  
 300  
 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA  
 360  
 GACAGGCCAG AATTGGCCAG CATGCTGGAC ATGGCCATGT TTCAGGACCC ACAGGAGCGA  
 65 420

	480	CCCAGAAAGT	TACCACAGTT	ATGCACAGAG	CTGCAAACAA	CTATACATGA	TATAATATTA
	540	GAATGTGTGT	ACTGCAAGCA	ACAGTTACTG	CGACGTGAGG	TATATGACTT	TGCTTTTCGG
5	600	GATTTATGCA	TAGTATATAG	AGATGGGAAT	CCATATGCTG	TATGTGATAA	ATGTTTAAAG
	660	TTTTATTCTA	AAATTAGTGA	GTATAGACAT	TATTGTTATA	GTTTGTATGG	AACAACATTA
10	720	GAACAGCAAT	ACAACAAACC	GTTGTGTGAT	TTGTTAATTA	GGTGTATTAA	CTGTCAAAAG
	780	CCACTGTGTC	CTGAAGAAAA	GCAAAGACAT	CTGGACAAAA	AGCAAAGATT	CCATAATATA
	840	AGGGGTCGGT	GGACCGGTCT	ATGTATGTCT	TGTTGCAGAT	CATCAAGAAC	ACGTAGAGAA
15	900	ACCCAGCTGA	TGCATGGAGA	TACACCTACA	TTGCATGAAT	ATATGTTAGA	TTTGCAACCA
	960	GAGACAACCT	ATCTCTACTG	TTATGAGCAA	TTAAATGACA	GCTCAGAGGA	GGAGGATGAA
20	1020	ATAGATGGTC	CAGCTGGACA	AGCAGAACCG	GACAGAGCCC	ATTACAATAT	TGTAACCTTT
	1080	TGTTGCAAGT	GTGACTCTAC	GCTTCGGTTG	TGCGTACAAA	GCACACACGT	AGACATTTCGT
	1140	ACTTTGGAAG	ACCTGTTAAT	GGGCACACTA	GGAATTGTGT	GCCCCATCTG	TTCTCAGAAA
25	1173	CCAACCTAGT	GCCACCATCA	CCATCACCAT	TAA		

(2) INFORMATION FOR SEQ ID NO:14:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 35 CLYTA E6E7 His HPV16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40	Met	Lys	Gly	Gly	Ile	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
	1				5					10					15	
	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
				20					25					30		
	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
			35					40					45			
45	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50						55					60				
	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
	65					70					75					80
	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
50					85					90					95	
	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr	Tyr
				100					105					110		
	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Leu	Ala	Ser	Met
			115					120					125			
55	Leu	Asp	Met	Ala	Met	Phe	Gln	Asp	Pro	Gln	Glu	Arg	Pro	Arg	Lys	Leu
	130						135					140				
	Pro	Gln	Leu	Cys	Thr	Glu	Leu	Gln	Thr	Thr	Ile	His	Asp	Ile	Ile	Leu
	145					150					155					160
	Glu	Cys	Val	Tyr	Cys	Lys	Gln	Gln	Leu	Leu	Arg	Arg	Glu	Val	Tyr	Asp
60					165						170				175	
	Phe	Ala	Phe	Arg	Asp	Leu	Cys	Ile	Val	Tyr	Arg	Asp	Gly	Asn	Pro	Tyr
				180					185					190		
	Ala	Val	Cys	Asp	Lys	Cys	Leu	Lys	Phe	Tyr	Ser	Lys	Ile	Ser	Glu	Tyr
			195					200					205			
65	Arg	His	Tyr	Cys	Tyr	Ser	Leu	Tyr	Gly	Thr	Thr	Leu	Glu	Gln	Gln	Tyr
	210						215					220				

(2) INFORMATION FOR SEQ ID NO:15:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60 (2) INFORMATION FOR SEQ ID NO:16:

65 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 228 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
Thioredoxin

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

	Met	Ser	Asp	Lys	Ile	Ile	His	Leu	Thr	Asp	Asp	Ser	Phe	Asp	Thr	Asp
	1				5					10					15	
50	Val	Leu	Lys	Ala	Asp	Gly	Ala	Ile	Leu	Val	Asp	Phe	Trp	Ala	Glu	Trp
				20					25					30		
	Cys	Gly	Pro	Cys	Lys	Met	Ile	Ala	Pro	Ile	Leu	Asp	Glu	Ile	Ala	Asp
			35					40					45			
	Glu	Tyr	Gln	Gly	Lys	Leu	Thr	Val	Ala	Lys	Leu	Asn	Ile	Asp	Gln	Asn
55		50					55					60				
	Pro	Gly	Thr	Ala	Pro	Lys	Tyr	Gly	Ile	Arg	Gly	Ile	Pro	Thr	Leu	Leu
	65					70					75					80
	Leu	Phe	Lys	Asn	Gly	Glu	Val	Ala	Ala	Thr	Lys	Val	Gly	Ala	Leu	Ser
				85						90					95	
60	Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala			
				100					105							

(2) INFORMATION FOR SEQ ID NO:18:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

5

	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
60	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA
120	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT
180	CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC
240	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT
300	CAAAGTTTAG	AAATGACAGA	AACTTTGAA	ACCATGGCCA	TGCATGGACC	TAAGGCAACA
360	TTGCAAGACA	TTGTATTGCA	TTTAGAGCCC	CAAAATGAAA	TTCCGTTTGA	CCTTCTAGGT
420	CACCAGCAAT	TAAGCGACTC	AGAGGAAGAA	AACGATGAAA	TAGATGGAGT	TAATCATCAA
480	CATTTACCAG	CCCGACGAGC	CGAACCACAA	CGTCACACAA	TGTTGTGTAT	GTGTTGTAAG
540	TGTGAAGCCA	GAATTGAGCT	AGTAGTAGAA	AGCTCAGCAG	ACGACCTTCG	AGCATTCCAG
600	CAGCTGTTTC	TGAACACCCT	GTCCTTTGTG	TGTCCGTGGT	GTGCATCCCA	GCAGACTAGT
660	GGCCACCATC	ACCATCACCA	TTAA			
684						

35

40

45	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5				10					15		
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
				20					25					30		
	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
50			35					40					45			
	Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
		50					55					60				
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
	65				70						75					80
55	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
					85					90					95	
	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met
				100					105					110		
	Ala	Met	His	Gly	Pro	Lys	Ala	Thr	Leu	Gln	Asp	Ile	Val	Leu	His	Leu
60			115					120					125			
	Glu	Pro	Gln	Asn	Glu	Ile	Pro	Val	Asp	Leu	Leu	Gly	His	Gln	Gln	Leu
		130					135					140				
	Ser	Asp	Ser	Glu	Glu	Glu	Asn	Asp	Glu	Ile	Asp	Gly	Val	Asn	His	Gln
	145					150					155					160
65	His	Leu	Pro	Ala	Arg	Arg	Ala	Glu	Pro	Gln	Arg	His	Thr	Met	Leu	Cys
					165					170					175	

60	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5					10					15	
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
			20						25					30		
65	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Ala	Asp	
			35					40					45			

	ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC
45	60	ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA
	120	CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC
	180	CGTTTGTAGTGG	TTATTCACGA	TCACCTTTTGA	GATGGCTTGA	CTGATGTTGC
50	240	CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT
	300	CAAAGTTTGTAG	AAATGACAGA	AAACTTTGAA	ACCATGGCGC	GCTTTGAGGA
	360	CGACCCTACA	AGCTACCTGA	TCTGTGCACG	GAACTGAACA	CTTCACTGCA
55	420	ATAACCTGTG	TATATTGCAA	GACAGTATTG	GAACTTACAG	AGGTATTTGA
	480	AAAGATTTTAT	TTGTGGTGTA	TAGAGACAGT	ATACCGCATG	CTGCATGCCA
60	540	GATTTTTTATT	CTAGAATTAG	AGAATTAAGA	CATTATTCAG	ACTCTGTGTA
	600	TTGGAAAAAC	TAACCTAACAC	TGGGTTATAC	AATTTATTAA	TAAGGTGCCT
	660	AAACCGTTGA	ATCCAGCAGA	AAACTTAGA	CACCTTAATG	AAAAACGACG
65	720					ATTTCAACA

ATAGCTGGGC ACTATAGAGG CCAGTGCCAT TCGTGCTGCA ACCGAGCAGC ACAGGAACGA  
 780  
 CTCCAACGAC GCAGAGAAAC ACAAGTAATG CATGGACCTA AGGCAACATT GCAAGACATT  
 840  
 5 GTATTGCATT TAGAGCCCCA AAATGAAATT CCGGTTGACC TTCTATGTCA CGAGCAATTA  
 900  
 AGCGACTCAG AGGAAGAAAA CGATGAAATA GATGGAGTTA ATCATCAACA TTTACCAGCC  
 960  
 CGACGAGCCG AACCACAACG TCACACAATG TTGTGTATGT GTTGTAAAGTG TGAAGCCAGA  
 1020  
 10 ATTGAGCTAG TAGTAGAAAG CTCAGCAGAC GACCTTCGAG CATTCCAGCA GCTGTTTCTG  
 1080  
 AACACCCTGT CCTTTGTGTG TCCGTGGTGT GCATCCCAGC AGACTAGTGG CCACCATCAC  
 1140  
 15 CATCACCATT AA  
 1152

## (2) INFORMATION FOR SEQ ID NO:23:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 25 Protein D1/3 E6 E7 His/ HPV 18

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30	Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
	1				5					10				15		
	Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
				20					25					30		
	Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
				35				40					45			
35	Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
		50				55						60				
	Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
	65					70					75					80
	Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
				85						90					95	
40	Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met
				100					105					110		
	Ala	Arg	Phe	Glu	Asp	Pro	Thr	Arg	Arg	Pro	Tyr	Lys	Leu	Pro	Asp	Leu
				115				120					125			
45	Cys	Thr	Glu	Leu	Asn	Thr	Ser	Leu	Gln	Asp	Ile	Glu	Ile	Thr	Cys	Val
		130				135						140				
	Tyr	Cys	Lys	Thr	Val	Leu	Glu	Leu	Thr	Glu	Val	Phe	Glu	Phe	Ala	Phe
	145					150						155				160
	Lys	Asp	Leu	Phe	Val	Val	Tyr	Arg	Asp	Ser	Ile	Pro	His	Ala	Ala	Cys
				165						170					175	
50	His	Lys	Cys	Ile	Asp	Phe	Tyr	Ser	Arg	Ile	Arg	Glu	Leu	Arg	His	Tyr
				180					185					190		
	Ser	Asp	Ser	Val	Tyr	Gly	Asp	Thr	Leu	Glu	Lys	Leu	Thr	Asn	Thr	Gly
				195				200					205			
55	Leu	Tyr	Asn	Leu	Leu	Ile	Arg	Cys	Leu	Arg	Cys	Gln	Lys	Pro	Leu	Asn
		210				215						220				
	Pro	Ala	Glu	Lys	Leu	Arg	His	Leu	Asn	Glu	Lys	Arg	Arg	Phe	His	Asn
						230						235				240
	Ile	Ala	Gly	His	Tyr	Arg	Gly	Gln	Cys	His	Ser	Cys	Cys	Asn	Arg	Ala
				245						250					255	
60	Arg	Gln	Glu	Arg	Leu	Gln	Arg	Arg	Arg	Glu	Thr	Gln	Val	Met	His	Gly
				260					265					270		
	Pro	Lys	Ala	Thr	Leu	Gln	Asp	Ile	Val	Leu	His	Leu	Glu	Pro	Gln	Asn
				275				280					285			
65	Glu	Ile	Pro	Val	Asp	Leu	Leu	Cys	His	Glu	Gln	Leu	Ser	Asp	Ser	Glu
		290					295						300			



